

SEQUENCE LISTING

<110> Nicolaides, Nicholas
Grasso, Luigi
Sass, Philip
Kinzler, Kenneth
Vogelstein, Bert

<120> A method for generating hypermutable
plants

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Val Glu Phe Lys Lys	Trp Gly Pro Val Leu Ala Phe Ile Glu Arg Ile	285
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Gly Ala Asp Ile Leu	Ala Lys Gly Asp Arg Gln Asp Leu Ile Asp Asp	320
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Pro Met Tyr Ser Thr	Pro Ser Ala Thr Lys Trp Glu Ser Glu Tyr Gln	640
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Lys Gly Cys Arg Ile	Leu Glu Gln Ser Leu Arg Leu Gly Arg Met Pro	655
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Glu Val Ile Pro Glu	Met Asp Cys Cys Glu Thr Gly Thr Asp Ser Phe	685
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755 760 765
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820 825 830
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      M E R A E S S S T E P A K A I K P I D R
1    ATG GAG CGA GCT GAG AGC TCG AGT ACA GAA CCT GCT AAG GCC ATC AAA CCT ATT GAT CGG
      K S V H Q I C S G Q V V L S L S T A V K
61   AAG TCA GTC CAT CAG ATT TGC TCT GGG CAG GTG GTA CTG AGT CTA AGC ACT GCG GTA AAG
      E L V E N S L D A G A T N I D L K L K D
121  GAG TTA GTA GAA AAC AGT CTG GAT GCT GGT GCC ACT AAT ATT GAT CTA AAG CTT AAG GAC
      Y G V D L I E V S D N G C G V E E E N F
181  TAT GGA GTG GAT CTT ATT GAA GTT TCA GAC AAT GGA TGT GGG GTA GAA GAA GAA AAC TTC
      E G L T L K H H T S K I Q E F A D L T Q
241  GAA GGC TTA ACT CTG AAA CAT CAC ACA TCT AAG ATT CAA GAG TTT GCC GAC CTA ACT CAG
      V E T F G F R G E A L S S L C A L S D V
301  GTT GAA ACT TTT GGC TTT CGG GGG GAA GCT CTG AGC TCA CTT TGT GCA CTG AGC GAT GTC
      T I S T C H A S A K V G T R L M F D H N
361  ACC ATT TCT ACC TGC CAC GCA TCG GCG AAG GTT GGA ACT CGA CTG ATG TTT GAT CAC AAT
      G K I I Q K T P Y P R P R G T T V S V Q
421  GGG AAA ATT CAT CAG AAA ACC CCC TAC CCC CGC AGA GGG ACC ACA GTC AGC GTG CAG
      Q L F S T L P V R H K E F Q R N I K K E
481  CAG TTA TTT TCC ACA CTA CCT GTG CGC CAT AAG GAA TTT CAA AGG AAT ATT AAG AAG GAG
      Y A K M V Q V L H A Y C I I S A G I R V
541  TAT GCC AAA ATG GTC CAG GTC TTA CAT GCA TAC TGT ATC ATT TCA GCA GGC ATC CGT GTA
      S C T N Q L G Q G K R Q P V V C T G G S
601  AGT TGC ACC AAT CAG CTT GGA CAA GGA AAA CGA CAG CCT GTG GTA TGC ACA GGT GGA AGC
      P S I K E N I G S V F G Q K Q L Q S L I
661  CCC AGC ATA AAG GAA AAT ATC GGC TCT GTG TTT GGG CAG AAG CAG TTG CAA AGC CTC ATT
      P F V Q L P P S D S V C E E Y G L S C S
721  CCT TTT GTT CAG CTG CCC CCT AGT GAC TCC GTG TGT GAA GAG TAC GGT TTG AGC TGT TCG
      D A L H N L F Y I S G F I S Q C T H G V
781  GAT GCT CTG CAT AAT CTT TTT TAC ATC TCA GGT TTC ATT TCA CAA TGC ACG CAT GGA GTT
      G R S S T D R Q F F F I N R R P C D P A
841  GGA AGG AGT TCA ACA GAC AGA CAG TTT TTC TTT ATC AAC CGG CGG CCT TGT GAC CCA GCA
      K V C R L V N E V Y H M Y N R H Q Y P F
901  AAG GTC TGC AGA CTC GTG AAT GAG GTC TAC CAC ATG TAT AAT CGA CAC CAG TAT CCA TTT
      V V L N I S V D S E C V D I N V T P D K
961  GTT GTT CTT AAC ATT TCT GTT GAT TCA GAA TGC GTT GAT ATC AAT GTT ACT CCA GAT AAA
      R Q I L L Q E E K L L L A V L K T S L I
1021 AGG CAA ATT TTG CTA CAA GAG GAA AAG CTT TTG TTG GCA GTT TTA AAG ACC TCT TTG ATA
      G M F D S D V N K L N V S Q Q P L L D V
1081 GGA ATG TTT GAT AGT GAT GTC AAC AAG CTA AAT GTC AGT CAG CAG CCA CTG CTG GAT GTT
      E G N L I K M H A A D L E K P M V E K Q
1141 GAA GGT AAC TTA ATA AAA ATG CAT GCA GCG GAT TTG GAA AAG CCC ATG GTA GAA AAG CAG
      D Q S P S L R T G E E K K D V S I S R L
1201 GAT CAA TCC CCT TCA TTA AGG ACT GGA GAA GAA AAA GAC GTG TCC ATT TCC AGA CTG
      R E A F S L R H T T E N K P H S P K T P
1261 CGA GAG GCC TTT TCT CTT CGT CAC ACA ACA GAG AAC AAG CCT CAC AGC CCA AAG ACT CCA
      E P R R S P L G Q K R G M L S S S T S G
1321 GAA CCA AGA AGG AGC CCT CTA GGA CAG AAA AGG GGT ATG CTG TCT TCT AGC ACT TCA GGT
      A I S D K G V L R P Q K E A V S S S H G
1381 GCC ATC TCT GAC AAA GGC GTC CTG AGA CCT CAG AAA GAG GCA GTG AGT TCC AGT CAC GGA
      P S D P T D R A E V E K D S G H G S T S
1441 CCC AGT GAC CCT ACG GAC AGA GCG GAG GTG GAG AAG GAC TCG GGG CAC GGC AGC ACT TCC
      V D S E G F S I P D T G S H C S S E Y A
1501 GTG GAT TCT GAG GGG TTC AGC ATT CCA GAC ACG GGC AGT CAC TGC AGC AGC GAG TAT GCG
      A S S P G D R G S Q E H V D S Q E K A P
1561 GCC AGC TCC CCA GGG GAC AGG GGC TCG CAG GAA CAT GTG GAC TCT CAG GAG AAA GCG CCT
      E T D D S F S D V D C H S N Q E D T G C
1621 GAA ACT GAC GAC TCT TTT TCA GAT GTG GAC TGC CAT TCA AAC CAG GAA GAT ACC GGA TGT
      K F R V L P Q P T N L A T P N T K R F K
1681 AAA TTT CGA GTT TTG CCT CAG CCA ACT AAT CTC GCA ACC CCA AAC ACA AAG CGT TTT AAA
      K E E I L S S S D I C Q K L V N T Q D M
1741 AAA GAA GAA ATT CTT TCC AGT TCT GAC ATT TGT CAA AAG TTA GTA AAT ACT CAG GAC ATG
      S A S Q V D V A V K I N K K V V P L D F
1801 TCA GCC TCT CAG GTT GAT GTA GCT GTG AAA ATT AAT AAG AAA GTT GTG CCC CTG GAC TTT
      S M S S L A K R I K Q L H H E A Q Q S E
1861 TCT ATG AGT TCT TTA GCT AAA CGA ATA AAG CAG TTA CAT CAT GAA GCA CAG CAA AGT GAA
      G E Q N Y R K F R A K I C P G E N Q A A
1921 GGG GAA CAG AAT TAC AGG AAG TTT AGG GCA AAG ATT TGT CCT GGA GAA AAT CAA GCA GCC
      E D E L R K E I S K T M F A E M E I I G
1981 GAA GAT GAA CTA AGA AAA GAG ATA AGT AAA ACG ATG TTT GCA GAA ATG GAA ATC ATT GGT
      Q F N L G F I I T K L N E D I F I V D Q
2041 CAG TTT AAC CTG GAT TTT ATA ATA ACC AAA CTG AAT GAG GAT ATC TTC ATA GTG CAG GAC
      H A T D E K Y N F E M L Q Q H T V L Q G
2101 CAT GCC ACG GAC GAG AAG TAT AAT TTC GAG ATG CTG CAG CAG CAC ACC GTG CTC CAG GGG
      Q R L I A P Q T L N L T A V N E A V L I
2161 CAG AGG CTC ATA GCA CCT CAG ACT CTC AAC TTA ACT GCT GTT AAT GAA GCT GTT CTG ATA
      E N L E I F R K N G F D F V I D E N A P
2221 GAA AAT CTG GAA ATA TTT AGA AAG AAT GGC TTT GAT TTT GTT ATC GAT GAA AAT GCT CCA

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      V   T   E   R   A   K   L   I   S   L   P   T   S   K   N   W   T   F   G   P
2281  GTC ACT GAA AGG GCT AAA CTG ATT TCC TTG CCA ACT AGT AAA AAC TGG ACC TTC GGA CCC
      Q   D   V   D   E   L   I   F   M   L   S   D   S   P   G   V   M   C   R   P
2341  CAG GAC GTC GAT GAA CTG ATC TTC ATG CTG AGC GAC AGC CCT GGG GTC ATG TGC CGG CCT
      S   R   V   K   Q   M   F   A   S   R   A   C   R   K   S   V   M   I   G   T
2401  TCC CGA GTC AAG CAG ATG TTT GCC TCC AGA GCC TGC CGG AAG TCG GTG ATG ATT GGG ACT
      A   L   N   T   S   E   M   K   K   L   I   T   H   M   G   E   M   D   H   P
2461  GCT CTT AAC ACA AGC GAG ATG AAG AAA CTG ATC ACC CAC ATG GGG GAG ATG GAC CAC CCC
      W   N   C   P   H   G   R   P   T   M   R   H   I   A   N   L   G   V   I   S
2521  TGG AAC TGT CCC CAT GGA AGG CCA ACC ATG AGA CAC ATC GCC AAC CTG GGT GTC ATT TCT
      Q   N   *
2581  CAG AAC TAG

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Sequence ID 3. Human PMS2 (ACCESSION U13696) cDNA and amino acid sequences.

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      M Q G D S S P S P T T T S S P L I R P I
1    ATG CAA GGA GAT TCT TCT CCG TCT CCG ACG ACT ACT AGC TCT CCT TTG ATA AGA CCT ATA
      N R N V I H R I C S G Q V I L D L S S A
61   AAC AGA AAC GTA ATT CAC AGA ATC TGT TCC GGT CAA GTC ATC TTA GAC CTC TCT TCG GCC
      V K E L V E N S L D A G A T S I E I N L
121  GTC AAG GAG CTT GTC GAG AAT AGT CTC GAC GCC GGC GCC ACC AGT ATA GAG ATT AAC CTC
      R D Y G E D Y F Q V I D N G C G I S P T
181  CGA GAC TAC GGC GAA GAC TAT TTT CAG GTC ATT GAC AAT GGT TGT GGC ATT TCC CCA ACC
      N F K V C V Q I L R R T F D V L A L K H
241  AAT TTC AAG GTT TGT GTC CAA ATT CTC CGA AGA ACT TTT GAT GTT CTT GCA CTT AAG CAT
      H T S K L E D F T D L L N L T T Y G F R
301  CAT ACT TCT AAA TTA GAG GAT TTC ACA GAT CTT TTG AAT TTG ACT ACT TAT GGT TTT AGA
      G E A L S S L C A L G N L T V E T R T K
361  GGA GAA GCC TTG AGC TCT CTC TGT GCA TTG GGA AAT CTC ACT GTG GAA ACA AGA ACA AAG
      N E P V A T L L T F D H S G L L T A E K
421  AAT GAG CCA GTT GCT AGC CTC TGT ACG TTT GAT CAT TCT GGT TTG CTT ACT GCT GAA AAG
      K T A R Q I G T T V T V R K L F S N L P
481  AAG ACT GCT CGC CAA ATT GGT ACC ACT GTC ACT GTT AGG AAG TTG TTC TCT AAT TTA CCT
      V R S K E F K R N I R K E Y G K L V S L
541  GTA CGA AGC AAA GAG TTT AAG CGG AAT ATA CGC AAA GAA TAT GGG AAG CTT GTA TCT TTA
      L N A Y A L I A K G V R F V C S N T T G
601  TTG AAC GCA TAT GGG CTT ATT GCG AAA GGA GTG CGG TTT GTC TCT AAC ACG ACT GGG
      K N P K S V V L N T Q G R G S L K D N I
661  AAA AAC CCA AAG TCT GTT GTG CTG AAC ACA CAA GGG AGG GGT TCA CTT AAA GAT AAT ATC
      I T V F G I S T F T S L Q P G T G R N L
721  ATA ACA GTT TTC GGC ATT AGT ACC TTT ACA AGT CTA CAG CCT GGT ACT GGA CGC AAT TTA
      A D R Q Y F F I N G R P V D M P K V S K
781  GCA GAT CGA CAG TAT TTC TTT ATA AAT GGT CGG CCT GTA GAT ATG CCA AAA GTC AGC AAG
      L V N E L Y K D T S S R K Y P V T I L D
841  TTG GTG AAT GAG TTA TAT AAA GAT ACA AGT TCT CGG AAA TAT CCA GTT ACC ATT CTG GAT
      F I V P G G A C D L N V T P D K R K V F
901  TTT ATT GTG CCT GGT GGA GCA TGT GAT TTG AAT GTC ACG CCC GAT AAA AGA AAG GTG TTC
      F S D E T S V I G S L R E G L N E I Y S
961  TTT TCT GAC GAG ACT TCT GTT ATC GGT TCT TTG AGG GAA GGT CTG AAC GAG ATA TAT TCC
      S S N A S Y I V N R F E E N S E Q P D K
1021 TCC AGT AAT GCG TCT TAT ATT GTT AAT AGG TTC GAG GAG AAT TCG GAG CAA CCA GAT AAG
      A G V S S F Q K S N L L S E G I V L D
1081 GCT GGA GTT TCG TCG TTT CAG AAG AAA TCA AAT CTT TTG TCA GAA GGG ATA GTT CTG GAT
      V S S K A T R L G E A I E K E N P S L R E
1141 GTC AGT TCT AAA ACA ASA CTA GGG GAA GCT ATT GAG AAA GAA AAT CCA TCC TTA AGG GAG
      V E I D N S S P M E K F K F E I K A C G
1201 GTT GAA ATT GAT AAT AGT TCG CCA ATG GAG AAG TTT AAG TTT GAG ATC AAG GCA TGT GGG
      T K K G E G S L S V H D V T H L D K T P
1261 ACG AAG AAA GGG GAA GGT TCT TTA TCA GTC CAT GAT GTA ACT CAC CTT GAC AAG ACA CCT
      S K G L P Q L N V T E K V T D A S K D L
1321 AGC AAA GGT TTG CCT CAG TTA AAT GTG ACT GAG AAA GTT ACT GAT GCA AGT AAA GAC TTG
      S S R S S F A Q S T L N T F V T M G K R
1381 AGC AGC CGC TCT AGC TTT GCC CAG TCA ACT TTG AAT ACT TTT GTT ACC ATG GGA AAA AGA
      K H E N I S T I L S E T P V L R N Q T S
1441 AAA CAT GAA AAC ATA AGC ACC ATC CTC TCT GAA ACA CCT GTC CTC AGA AAC CAA ACT TCT
      S Y R V E K S K F E V R A L A S R C L V
1501 AGT TAT CGT GTG GAG AAA AGC AAA TTT GAA GTT CGT GCC TTA GCT TCA AGG TGT CTC GTG
      E G D Q L D D M V I S K E D M T P S E R
1561 GAA GGC GAT CAA CTT GAT GAT ATG GTC ATC TCA AAG GAA GAT ATG ACA CCA AGC GAA AGA
      D S E L G N R I S P G T Q A D N V E R H
1621 GAT TCT GAA CTA GGC AAT CGG ATT TCT CCT GGA ACA CAA GCT GAT AAT GTT GAA AGA CAT
      E R V L G Q F N L G F I I A K L E R D L
1681 GAG AGA GTA CTC GGG CAA TTC AAT CTT GGG TTC ATC ATT GCA AAA TTG GAG CGA GAT CTG
      F I V D Q H A A D E K F N F E H L A R S
1741 TTC ATT GTG GAT CAG CAT GCA GCT GAT GAG AAA TTC AAC TTC GAA CAT TTA GCA AGG TCA
      T V L N Q Q P L L Q P L N L E L S P E E
1801 ACT GTC CTG AAC CAG CAA CCC TTA CTC CAG CCT TTG AAC TTG GAA CTC TCT CCA GAA GAA
      E V T V L M H M D I I R E N G F L L E E
1861 GAA GTA ACT GTG TTA ATG CAC ATG GAT ATT ATC AGG GAA AAT GGC TTT CTT CTA GAG GAG
      N P S A P P G K H F R L R A I P Y S K N
1921 AAT CCA AGT GCT CCT CCC GGA AAA CAC TTT AGA CTA CGA GCC ATT CCT TAT AGC AAG AAT
      I T F G V E D L K D L I S T L G D N H G
1981 ATC ACC TTT GGA GTC GAA GAT CTT AAA GAC CTG ATC TCA ACT CTA GGA GAT AAC CAT GGG
      E C S V A S S Y K T S K T D S I C P S R
2041 GAA TGT TCG GTT GCT AGT AGC TAC AAA ACC AGC AAA ACA GAT TCG ATT TGT CCA TCA CGA
      V R A M L A S R A C R S S V M I G D P L
2101 GTC CGT GCA ATG CTA GCA TCC CGA GAT TGC AGA TCA TCT GTG ATG ATC GGA GAT CCA CTC
      R K N E M Q K I V E H L A D L E S P W N
2161 AGA AAA AAC GAA ATG CAG AAG ATA GTA GAA CAC TTG GCA GAT CTC GAA TCT CCT TGG AAT
      C P H G R P T M R H L V D L T T L L T L
2221 TGC CCA CAC GGA CGA CCA ATG CGT CAT CTT GTG GAC TTG ACA ACT TTA CTC ACA TTA
      P D D D N V N D D D D D A T I S L A *

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2281 CCT GAT GAC GAC AAT GTC AAT GAT GAT GAT GAT GAT GAT GCA ACC ATC TCA TTG GCA TGA

Sequence ID 4. *Arabidopsis thaliana* PMS2 homologue (ACCESSION AF069298) cDNA and amino acid sequenc.

M E R A E S S S T E P A K A I K P I D R
 1 ATG GAG CGA GCT GAG AGC TCG AGT ACA GAA CCT GCT AAG GCC ATC AAA CCT ATT GAT CGG
 K S V H Q I C S G Q V V L S L S T A V K
 61 AAG TCA GTC CAT CAG ATT TGC TCT GGG CAG GTG GTA CTG AGT CTA AGC ACT GCG GTA AAG
 E L V E N S L D A G A T N I D L K L K D
 121 GAG TTA GTA GAA AAC AGT CTG GAT GCT GGT GCC ACT AAT ATT GAT CTA AAG CTT AAG GAC
 Y G V D L I E V S D N G C G V E E E N F
 181 TAT GGA GTG GAT CTT ATT GAA GTT TCA GAC AAT GGA TGT GGG GTA GAA GAA GAA AAC TTC
 E G L T L K H H T S K I Q E F A D L T Q
 241 GAA GGC TTA ACT CTG AAA CAT CAC ACA TCT AAG ATT CAA GAG TTT GCC GAC CTA ACT CAG
 V E T F G F R G E A L S S L C A L S D V
 301 GTT GAA ACT TTT GGC TTT CGG GGG GAA GCT CTG AGC TCA CTT TGT GCA CTG AGC GAT GTC
 T I S T C H A S A K V G T *
 361 ACC ATT TCT ACC TGC CAC GCA TCG GCG AAG GTT GGA ACT TAG

Sequence ID 5. Human PMS134 cDNA and amino acid sequences.

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      M  Q  G  D  S  S  P  S  P  T  T  T  S  S  P  L  I  R  P  I
1    ATG CAA GGA GAT TCT TCT CCG TCT CCG ACG ACT ACT AGC TCT CCT TTG ATA AGA CCT ATA
    N  R  N  V  I  H  R  I  C  S  G  Q  V  I  L  D  L  S  S  A
61   AAC AGA AAC GTA ATT CAC AGA ATC TGT TCC GGT CAA GTC ATC TTA GAC CTC TCT TCG GCC
    V  K  E  L  V  E  N  S  L  D  A  G  A  T  S  I  E  I  N  L
121  GTC AAG GAG CTT GTC GAG AAT AGT CTC GAC GCC GGC GCC ACC AGT ATA GAG ATT AAC CTC
    R  D  Y  G  E  D  Y  F  Q  V  I  D  N  G  C  G  I  S  P  T
181  CGA GAC TAC GGC GAA GAC TAT TTT CAG GTC ATT GAC AAT GGT TGT GGC ATT TCC CCA ACC
    N  F  K  V  C  V  Q  I  L  R  R  T  F  D  V  L  A  L  K  H
241  AAT TTC AAG GTT TGT GTC CAA ATT CTC CGA AGA ACT TTT GAT GTT CTT GCA CTT AAG CAT
    H  T  S  K  L  E  D  F  T  D  L  L  N  L  T  T  Y  G  F  R
301  CAT ACT TCT AAA TTA GAG GAT TTC ACA GAT CTT TTG AAT TTG ACT ACT TAT GGT TTT AGA
    G  E  A  L  S  S  L  C  A  L  G  N  L  T  V  E  T  R  T  K
361  GGA GAA GCC TTG AGC TCT CTC TGT GCA TTG GGA AAT CTC ACT GTG GAA ACA AGA ACA AAG
    N  E  P  V  A  T  L  *
421  AAT GAG CCA GTT GCT ACG CTC ...

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Sequence ID 6. *Arabidopsis thaliana* PMS134 homologue cDNA and amino acid sequences.

	1		70
humPMS2	(1)	ATGCAAGCGAGCTGAGAGCTCCAGCAGACAACCTGTCTAAGGCC-----ATCAAACCTTATGCATCGGAAGT	
AtPMS2	(1)	ATGCAAGAGACTTCCTCTCCGCTCCGACGACTACTGCTCTCTTTGATAAGCACTTAAACCAATCG	
Consensus		ATG A GAG T CG T C CT CTA C AT A ACCTTAT A G AA	
	71		140
humPMS2	(65)	CAGTCCATCAGATTTCCTCTGCGCACGTGGTACTGAGTCTAAGCACTGGCTAAAGGAGTCTAGTAGAAA	
AtPMS2	(71)	TAAATTCACAGAATCTGTTCCGCTCAAGTCACCTTAGACTCTCTTTCGCGCTCAAGGAGCTTTTCGAGAA	
Consensus	(71)	A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA	
	141		210
humPMS2	(135)	CAGTCTGATCTCTGTCGCCATCATATGATCTAAAGCTTAAGCACTATGGAGTGATCTATTCTCAAGTT	
AtPMS2	(141)	TAGTCTCGACGCGCGCGCCACCATATAGAGATTAACTCCGAGACTACGGCAAGACTATTCTCAGTCT	
Consensus	(141)	AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT	
	211		280
humPMS2	(205)	TCAGACAATGCATGTGGGTTTT-----AGAAGAAG-----AAAACTTCGAAG-----G	
AtPMS2	(211)	ATTCACAATGCTGTGGCCATTTCGCCAACCAATTTCAAGGTTTGTGTCCAATTTCCGGAAGCACTTTTG	
Consensus	(211)	GACAATGG TTGG T A AAG AA CT CGAAG G	
	281		350
humPMS2	(246)	CTTAACCT---CTGAACATCACAGATCTAAGA--TCAAGCTTTGGCCAGCTTAACCTGCGTTGA--ACT-	
AtPMS2	(281)	ATGTTCTTGCACTTAAGCATCATCACTCTTAATATAGAGGATTTACAGACTCTTT-TCAATCTGACTACT	
Consensus	(281)	T CT CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT	
	351		420
humPMS2	(311)	TTGGCTTTCCGGGGGAAGCTCTGAGCTCACTTTGTGCATCGA--CGATGTCACTATTCTCACT--CTC--	
AtPMS2	(350)	ATGGTTTTTAGAGGAGAAGGCTTGAAGCTCTCTGTGTGCAITGGGAAATCTCACTGTGGAA--AAAGAGAA	
Consensus	(351)	TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A	
	421		490
humPMS2	(379)	GCATCGGCGAAGCTTGAAGCTGACTGATGTTTGTATCACAATGGGAAATTA--TCCAGAA--ACCCCCTAC	
AtPMS2	(420)	GATAGAGCA--GTTGCTACGCTCTGTCAGTTTGATCATTTCTGGTTTGGTTAATGCTGAA--AGAAGACTG	
Consensus	(421)	G AT CC A GTTG AC C TGA GTTGATCA TGG TTA T C GARAA	
	491		560
humPMS2	(448)	CTCGCGCGAAGGACCACAGCTCAGCTGTCAGCTTAATTTCCACACTTACCTGTGCCCCATAGAGAA-	
AtPMS2	(488)	CTC-GCCAAATTTGGTACCACCTCTCACTTTAGCAAGTTGTTCTCTTAATTACCTGTACCAAGCAAGAG-	
Consensus	(491)	C C GCC A GG ACCAC GTCA GT G AGTT TT TC A TACCTGT CG AA GA T	
	561		630
humPMS2	(518)	TTCAAGGAATATTAAGAAGGACTATGCCAAATGTTCCAGGCTTACATGSCATACTGTATCATTTAGC	
AtPMS2	(557)	TTAAGCGGAATATACGCAAGAAATATGGGAAGCTTGTATCTTTATTGAACSCATATGCGCTATTGGAA	
Consensus	(561)	TT A GGAATAT AA GA TATG AA T GT T TT A GCATA T ATT C	
	631		700
humPMS2	(588)	AGGCATCTGCTGAAGTTGCAACCTCACTTGGACAGGAAGAAAGCAAGGCTGTGCTATGCACAGGTGGA	
AtPMS2	(627)	AGGAGTCCGTTTGTCTGCTTACACACTCTGGGAA--AACCAAGCTCTGTGTC--CTCTG	
Consensus	(631)	AGG T CGG T TGC C AA G TGG AA AA C A AG CTGT GT G GA	
	701		770
humPMS2	(658)	AGCCCCAGCATTAAGAGGAATATCGGCTCTGTGTTTGGCAGAAAGCAGTTGCAAAGCCTCATTCCTTTTG	
AtPMS2	(686)	A--CA-CACAA-GGG--G-G-	
Consensus	(701)	A CA CA AA GG A G G	
	771		840
humPMS2	(728)	TTCAAGTCCCTCTAGTGAATCCGCTGTGTAAGAGTACGGTTTGAAGCTGTCGGATGCTCTGCATATCT	
AtPMS2	(702)	TTCA-----GT-TAAGA--TAAT-----ATCATTAACAGTTT-----TCGCATTAGTA	
Consensus	(771)	TTCA C TA GA T A A AC GTTT TC GCAT A	
	841		910
humPMS2	(798)	TTTTTACATCTCAGGTTTTCATTTCAAAATGCAACGATGGAGTTGGAAGGAGTTTCAACAGACAGACAGTT	
AtPMS2	(743)	COITTACAGCT-----TACA-GCTGTACTGGAACCAATTTAGCAGTTCGACAGTA-	
Consensus	(841)	TTTACA TC T CA GC TGG TGA G A TT A CAGA GACAGT T	
	911		980
humPMS2	(868)	TTCTTTTATCAACCGCGGCCCTGTGACCCAGCAAAAGGCTGCAAGCTCGTGAATCAGGCTCACCACATG-	
AtPMS2	(796)	TTCTTTTAAATGCTCGGCCTGTATATATGCCAAAGATGCAAGCTGTTGAATGACTATAT--AAAG-	
Consensus	(911)	TTCTTTTAT AA G CGGCT GA CAAA GTC GCA T GTGAATGAG T TA A A T	
	981		1050
humPMS2	(938)	ATAA--TCGACACCACTATCCATTTGTTGTTCTTAACATTTCTGTTGATTCGAATGCGTGTATATCAATG	
AtPMS2	(865)	ACAAGTTCTCGGAATATCCACTACCATTTCTGGAATTTATCTGCGCTGGTGGAGCATGCTATTGATG	
Consensus	(981)	A AA T C A TATCCA TT TTCT A TT TGT T G A TGAT T AATG	
	1051		1120
humPMS2	(1007)	TTACTCCAGATAAAAGGCAAAATTTGCAACACAGGAAAGCTTTTCTTGGCACTTTTAAAGACCTCTTT	
AtPMS2	(935)	TACGCGCCGATAAAAGAAAGGCTCTCTTCTGCGAGA--CTTCTGTTATCTGTT-----CTTT	
Consensus	(1051)	T AC CC GATAAAG A T TT T GA GA A CTT TGTT G GTT CTTT	
	1121		1190
humPMS2	(1077)	GATAGGAATGTTTGATAGTGATGTCAAGAGCTAAATGTGAGTCAGCAGCCCACTGCTGGAAGTTGAGGGT	
AtPMS2	(993)	GAG-GGAAGGCTCA-----A-CGATATATTCG--T-CCAGTAATCCGCTTAT---	
Consensus	(1121)	GA GGAA GT TGA A C AG TA AT C T CCA T TG T TT A	
	1191		1260
humPMS2	(1147)	AACTTAATAAATAATCATGCACCGCATTTCGAAAGACCCATGTTAGAAAGCAGGATCAATCCCGTTGAT	
AtPMS2	(1040)	----TGTGTAATAGCTTGAGGACAAATTCGAGGCAACC--AGATAAG--GCGTGGTTCTGCTGT	
Consensus	(1191)	T T AA A T C G G G ATT GGA A CC AGA AAG G T A C TC T	
	1261		1330
humPMS2	(1217)	TAAAGGACTGGAGAAGAAAAAAGACGTGTGCATTTCAGACTGCCAGAGGCCCTTTTCTCTTCGTCAAC	
AtPMS2	(1097)	TTT-----AAGAAGAAATCAAA--TCTTTTGTCAAG--GGGATAG--TTCTGGATCTCAGTT	

Consensus (1261) T AGAAGAAA AAA TC TT CAGA G GA AG TTCT GTCA 1400
 humPMS2 (1287) AACAGAGAACAGCCTCACAGCCCAAGACCCAGAACCAAGAGGAGCCCTCTAGGACAGAAAAGGGGT 1470
 AtPMS2 (1148) CTAA---AACAGACT---AGGGGAAGCTATTGAGAGAGAAATCCCTTCTAAGGGAGTTGAAATTGA
 Consensus (1331) A AACAG CT AGG AA T AGAA AA A A CC T GGA AA G 1470
 humPMS2 (1357) ATGCTGTCTTCTGCACTTCAAGTGGCATCTCTACAAAGGCGTCCTGACAGCTCAGAAAGAGGCAGTGA 1540
 AtPMS2 (1212) TAATAGTTCCGCAATGGAGAAGTTAAGTTTGAATCAGGCATG-TGCGACGA-ACAAACGGCAAG---
 Consensus (1401) GT C A AG T T T GA AAGGC T TG GAC AGAAAG GG AG 1540
 humPMS2 (1427) GTTCAGTTCACGACCCAGTGACCCCTACGGACAGAGCGGAGGTGGAGAAAGAGTTCGGGCGACCGCAGCAC 1610
 AtPMS2 (1277) GTTCT--TTT-----CAGT---CCAT--GATGTATTCACCTTCACAAAG-ACACCTAGCAAAAGGTTTGC
 Consensus (1471) GTTC T A CAGT CC GA A C A T GA AAG AC C GCA G C 1610
 humPMS2 (1497) TTCCCTGGTTCCTGAGGGGTTTCAGCATCCAGACACGGGCGAGTCACTGCAGGACCGAGTATGCGGCGCGC 1680
 AtPMS2 (1334) CTCAGTTAATGTGACTG-----AGA-----AGTTACTGATGCA--AGTA-----TAG
 Consensus (1541) TC GT A T TGA G AGA AGT ACTG GCA AGTA A 1680
 humPMS2 (1567) TCCCGAGGGGACAGGGGCTCGCAGGAACATCTGGAATCTCAGGAGAAAGCGCTGAAACTGACCACTCTT 1750
 AtPMS2 (1376) AGTTGAG---CAGCCCTCT---A-GCTTGGCCAGTCA-----ACTT---TGAATACTTTT
 Consensus (1611) C AG CAG GCTC A T TG C TCA CT TGA ACT TT 1750
 humPMS2 (1637) TTTCAGATCTGGACTGCCATTCAAAACAGGAAGATCTGGATGTAAATTTTCAGAGTTTGTCTCAGCCAAC 1820
 AtPMS2 (1423) GTTACCATTGG-----AAA-----AAGAAAG--ATCAAAA-----CATAGCC--AG
 Consensus (1681) TT ATG G AAA AAGA A C ATG AAA C T AGC AC 1820
 humPMS2 (1707) TAAATTCGGAACCCCAACACAAAGCGTTTAAAAAAGAGAAATTCCTTCCAGTTCTGACATTTGTCTAA 1890
 AtPMS2 (1461) CATCTCTCTG-----AAACACT---GTCCACAGAAACCA-AACTTC-----AGTTAT--CGGTGGGAGA
 Consensus (1751) A CTC C AAAC C GT T A AAA A AA TTCT AGTT T C T TG A 1890
 humPMS2 (1777) AAGTTAGTAAATACTCAGGACATCTCAGCCTCTCAGGTTGATGTAGCTGTGAAAAATTAATAAGAAAGTTG 1960
 AtPMS2 (1517) AA---AGCAAAATTGAAGTTCTGTC-----CTTAGCTTCA--AGGTCG---CCCGT---GCAAGGCC
 Consensus (1821) AA AG AAAT AG C TG CT AG TT A AG TGT T T G AAG G 1960
 humPMS2 (1847) TGCCCTGGACTTTTCTATCAGTTCTTATGCTAAACCAATAAAGAGTTTACATCATCAAGCACAGCAAAAG 2030
 AtPMS2 (1568) ATCAACTTGA---GATATG-C---TCTCTCAAAG-----GAGATATGACCAAGGG---AAAG
 Consensus (1891) C CT GA T TATG G T A CT AA G G AG TA CA AAGC AAAG 2030
 humPMS2 (1917) TGAAGGGGAACAGAAATTAACGAAGTTTAGGCAAAAGTTTCTCCTGGAAGAAATCAAGCAGCCGGAATAT 2100
 AtPMS2 (1620) AATTTCTTAAT-----ACCGAATC-E-----GATTTCTCCTGGAAC--CAAGCTCATAATTTT
 Consensus (1961) G GAAC AGG A T G GATTT TCTTGA A CAAGC G A G T 2100
 humPMS2 (1987) GAACTAAGAAAGAGATTAATAAAACGATGTTTGAGAAATGGAATCATTTGGTCAGTTTAACTTGGAT 2170
 AtPMS2 (1672) GAA---AGACATGAGACA-STA---C-----TCCGGCAATTCAATCTTGGGT
 Consensus (2031) GAA AGA A GAGA A GTA C T GG CA TT AA CT GG T 2170
 humPMS2 (2057) TATAATAACCAAACTCAATGAGGATATCTTCATAGTGAACAGCATGCGACGACGAGAAAGTATACTTT 2240
 AtPMS2 (1712) TCACTATTGCAAAATTGAGCGGAGATCTGTTCAATCTGGATCAGCATGAGCTGATGAGAAATTCACCTT
 Consensus (2101) T AT AT C AAA TG A GAT T TTCAT GTGA CAGCATGC C GA GAGAA T AACTT 2240
 humPMS2 (2127) CGAG-ATGCTGCAACAGCACAGCTGCTCCAGGGGCGAGGCTCTATAGCA-CCTCAGACTCTCACTTAA 2310
 AtPMS2 (1782) CGAATTTTGAAGAGTCA-AGTCTCTGAAACCAACG-ACCTTTACTCAGCCTTTGAACTTGGACCTCT
 Consensus (2171) CGA AT GCA CA AC GT CT A GCA A CT A CA CCT GA T A T 2310
 humPMS2 (2195) CTGCTCTTAATGAAGCTGTCTCTGATAGAAATCTCGGAATATTTAGAAACAAATGGCTTTGATTTCTTTAT 2380
 AtPMS2 (1850) CTCCAGAACAGAGAAGTAACCTGCTTTAATGCACTAGGTATTATCAGGGGAAATGGCTTTCTTCTAAGGA
 Consensus (2241) CT C G A GAAG T TG TA A TGA AT T AG A AATGGCTTT T T G 2380
 humPMS2 (2265) CCATGAAATGCTCCAGTCACTGAAAGGGCT--AAACTGATTTCCTTGCCAACTAGTAAAACTGGACCT 2450
 AtPMS2 (1920) GAATCCAACTGCTCC--TCCGGGAAACACTTTAGCTACGAGCGATTCGTTATAGCAAGATATCACCT
 Consensus (2311) AT AA TGCTCC TC C GAAA CT A ACT CC T CC TAG AA AA ACCT 2450
 humPMS2 (2333) TCCGACCCCGGACGTGATCAACTGATCTTCATCTGAGCAGACCCCTCGGG-----TCATCTGCGCG 2520
 AtPMS2 (1988) TTGGAGTCCAGATCTTAAAGACCTGATCTCACTCTAGGAGATACCATGGGGAAATGTTGGGTGTGTAG 2590
 Consensus (2381) T GGA C A GA T A GA CTGATCT A CT G A CA CC TGGG TC TGC G 2520
 humPMS2 (2398) -----CCTTCCGAGTCAAGCAGATGTTTGGCTCCAGAGCC 2660
 AtPMS2 (2058) TAGCTACAAAACAGCAAAACAGATTGATTTGTCCATCAGAGTCCGTGCAATGCTAGCATCCGAGGA
 Consensus (2451) CC TC CGAGTC ATG T GC TCC GAGC 2660
 humPMS2 (2434) TCCCGAACTCGGTGATGATTTGGGACTCTCTTAAACAAGCGAGATGAAGAAACTGATCACCACATGG 259
 AtPMS2 (2128) TCGACATCATCTGTGATGATCCGAGATCCACTCAGAAACCAATGCAAGCATAGTAGAACACTTGG
 Consensus (2521) TGC G TC GTGATGAT GG T C CT A A AA CGA ATG AGAA T T CAC TGG 259
 humPMS2 (2504) GGGAGATGACCACCCCTGGAACTGTCCCATGGAAGGCCAACCATGAAACACATCCCCACCTGGGTGT 2660
 AtPMS2 (2198) CAGATCTCGAATCTCCTTGAATTCGCCACACCGAACCAACCAATGCTCATCTTGTGGACTTCACAA-
 Consensus (2591) GA T GA CC TGGAA TG CC CA GGA G CCAAC ATG G CA T G AC TG 2660